



## SEQUENCE LISTING

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<120> CRYSTAL STRUCTURE OF BACE AND USES  
THEREOF

<130> 16163-015001

<140> US 09/955,737

<141> 2001-09-19

<150> US 60/234,576

<151> 2000-09-22

<160> 6

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 501

<212> PRT

<213> Homo sapiens

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Gly	Leu	Gly	Gly	Ala	Pro	Leu	Gly	Leu	Arg	Leu	Pro	Arg	Glu	Thr	Asp
		35					40					45			
Glu	Glu	Pro	Glu	Glu	Pro	Gly	Arg	Arg	Gly	Ser	Phe	Val	Glu	Met	Val
	50					55					60				
Asp	Asn	Leu	Arg	Gly	Lys	Ser	Gly	Gln	Gly	Tyr	Tyr	Val	Glu	Met	Thr
65					70				75					80	
Val	Gly	Ser	Pro	Pro	Gln	Thr	Leu	Asn	Ile	Leu	Val	Asp	Thr	Gly	Ser
				85					90					95	
Ser	Asn	Phe	Ala	Val	Gly	Ala	Ala	Pro	His	Pro	Phe	Leu	His	Arg	Tyr
			100					105					110		
Tyr	Gln	Arg	Gln	Leu	Ser	Ser	Thr	Tyr	Arg	Asp	Leu	Arg	Lys	Gly	Val
		115					120					125			
Tyr	Val	Pro	Tyr	Thr	Gln	Gly	Lys	Trp	Glu	Gly	Glu	Leu	Gly	Thr	Asp
	130					135					140				
Leu	Val	Ser	Ile	Pro	His	Gly	Pro	Asn	Val	Thr	Val	Arg	Ala	Asn	Ile
145					150				155					160	
Ala	Ala	Ile	Thr	Glu	Ser	Asp	Lys	Phe	Phe	Ile	Asn	Gly	Ser	Asn	Trp
				165				170					175		
Glu	Gly	Ile	Leu	Gly	Leu	Ala	Tyr	Ala	Glu	Ile	Ala	Arg	Pro	Asp	Asp
			180					185					190		

Ser Leu Glu Pro Phe Phe Asp Ser Leu Val Lys Gln Thr His Val Pro  
 195 200 205  
 Asn Leu Phe Ser Leu Gln Leu Cys Gly Ala Gly Phe Pro Leu Asn Gln  
 210 215 220  
 Ser Glu Val Leu Ala Ser Val Gly Gly Ser Met Ile Ile Gly Gly Ile  
 225 230 235 240  
 Asp His Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr Pro Ile Arg Arg  
 245 250 255  
 Glu Trp Tyr Tyr Glu Val Ile Ile Val Arg Val Glu Ile Asn Gly Gln  
 260 265 270  
 Asp Leu Lys Met Asp Cys Lys Glu Tyr Asn Tyr Asp Lys Ser Ile Val  
 275 280 285  
 Asp Ser Gly Thr Thr Asn Leu Arg Leu Pro Lys Lys Val Phe Glu Ala  
 290 295 300  
 Ala Val Lys Ser Ile Lys Ala Ala Ser Ser Thr Glu Lys Phe Pro Asp  
 305 310 315 320  
 Gly Phe Trp Leu Gly Glu Gln Leu Val Cys Trp Gln Ala Gly Thr Thr  
 325 330 335  
 Pro Trp Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu Met Gly Glu Val  
 340 345 350  
 Thr Asn Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr Leu Arg  
 355 360 365  
 Pro Val Glu Asp Val Ala Thr Ser Gln Asp Asp Cys Tyr Lys Phe Ala  
 370 375 380  
 Ile Ser Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val Ile Met Glu  
 385 390 395 400  
 Gly Phe Tyr Val Val Phe Asp Arg Ala Arg Lys Arg Ile Gly Phe Ala  
 405 410 415  
 Val Ser Ala Cys His Val His Asp Glu Phe Arg Thr Ala Ala Val Glu  
 420 425 430  
 Gly Pro Phe Val Thr Leu Asp Met Glu Asp Cys Gly Tyr Asn Ile Pro  
 435 440 445  
 Gln Thr Asp Glu Ser Thr Leu Met Thr Ile Ala Tyr Val Met Ala Ala  
 450 455 460  
 Ile Cys Ala Leu Phe Met Leu Pro Leu Cys Leu Met Val Cys Gln Trp  
 465 470 475 480  
 Arg Cys Leu Arg Cys Leu Arg Gln Gln His Asp Asp Phe Ala Asp Asp  
 485 490 495  
 Ile Ser Leu Leu Lys  
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<210> 2

<211> 695

<212> PRT

<213> Homo sapiens

<400> 2

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 Ala Leu Glu Val Pro Thr Asp Gly Asn Ala Gly Leu Leu Ala Glu Pro  
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 Gln Ile Ala Met Phe Cys Gly Arg Leu Asn Met His Met Asn Val Gln  
 35 40 45  
 Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp  
 50 55 60  
 Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu  
 65 70 75 80

Gln	Ile	Thr	Asn	Val	Val	Glu	Ala	Asn	Gln	Pro	Val	Thr	Ile	Gln	Asn	
				85					90					95		
Trp	Cys	Lys	Arg	Gly	Arg	Lys	Gln	Cys	Lys	Thr	His	Pro	His	Phe	Val	
			100					105						110		
Ile	Pro	Tyr	Arg	Cys	Leu	Val	Gly	Glu	Phe	Val	Ser	Asp	Ala	Leu	Leu	
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Val	Pro	Asp	Lys	Cys	Lys	Phe	Leu	His	Gln	Glu	Arg	Met	Asp	Val	Cys	
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Glu	Thr	His	Leu	His	Trp	His	Thr	Val	Ala	Lys	Glu	Thr	Cys	Ser	Glu	
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Lys	Ser	Thr	Asn	Leu	His	Asp	Tyr	Gly	Met	Leu	Leu	Pro	Cys	Gly	Ile	
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Asp	Lys	Phe	Arg	Gly	Val	Glu	Phe	Val	Cys	Cys	Pro	Leu	Ala	Glu	Glu	
		180						185					190			
Ser	Asp	Asn	Val	Asp	Ser	Ala	Asp	Ala	Glu	Glu	Asp	Asp	Ser	Asp	Val	
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Trp	Trp	Gly	Gly	Ala	Asp	Thr	Asp	Tyr	Ala	Asp	Gly	Ser	Glu	Asp	Lys	
	210					215					220					
Val	Val	Glu	Val	Ala	Glu	Glu	Glu	Glu	Val	Ala	Glu	Val	Glu	Glu	Glu	
225					230					235					240	
Glu	Ala	Asp	Asp	Asp	Glu	Asp	Asp	Glu	Asp	Gly	Asp	Glu	Val	Glu	Glu	
			245					250						255		
Glu	Ala	Glu	Glu	Pro	Tyr	Glu	Glu	Ala	Thr	Glu	Arg	Thr	Thr	Ser	Ile	
		260						265					270			
Ala	Thr	Thr	Thr	Thr	Thr	Thr	Thr	Glu	Ser	Val	Glu	Glu	Val	Val	Arg	
	275						280					285				
Val	Pro	Thr	Thr	Ala	Ala	Ser	Thr	Pro	Asp	Ala	Val	Asp	Lys	Tyr	Leu	
	290					295					300					
Glu	Thr	Pro	Gly	Asp	Glu	Asn	Glu	His	Ala	His	Phe	Gln	Lys	Ala	Lys	
305				310					315						320	
Glu	Arg	Leu	Glu	Ala	Lys	His	Arg	Glu	Arg	Met	Ser	Gln	Val	Met	Arg	
			325					330						335		
Glu	Trp	Glu	Glu	Ala	Glu	Arg	Gln	Ala	Lys	Asn	Leu	Pro	Lys	Ala	Asp	
	340							345					350			
Lys	Lys	Ala	Val	Ile	Gln	His	Phe	Gln	Glu	Lys	Val	Glu	Ser	Leu	Glu	
	355						360					365				
Gln	Glu	Ala	Ala	Asn	Glu	Arg	Gln	Gln	Leu	Val	Glu	Thr	His	Met	Ala	
	370				375						380					
Arg	Val	Glu	Ala	Met	Leu	Asn	Asp	Arg	Arg	Arg	Leu	Ala	Leu	Glu	Asn	
385				390					395						400	
Tyr	Ile	Thr	Ala	Leu	Gln	Ala	Val	Pro	Pro	Arg	Pro	Arg	His	Val	Phe	
			405					410						415		
Asn	Met	Leu	Lys	Lys	Tyr	Val	Arg	Ala	Glu	Gln	Lys	Asp	Arg	Gln	His	
		420						425					430			
Thr	Leu	Lys	His	Phe	Glu	His	Val	Arg	Met	Val	Asp	Pro	Lys	Lys	Ala	
	435						440					445				
Ala	Gln	Ile	Arg	Ser	Gln	Val	Met	Thr	His	Leu	Arg	Val	Ile	Tyr	Glu	
	450					455					460					
Arg	Met	Asn	Gln	Ser	Leu	Ser	Leu	Leu	Tyr	Asn	Val	Pro	Ala	Val	Ala	
465				470					475						480	
Glu	Glu	Ile	Gln	Asp	Glu	Val	Asp	Glu	Leu	Leu	Gln	Lys	Glu	Gln	Asn	
			485					490						495		
Tyr	Ser	Asp	Asp	Val	Leu	Ala	Asn	Met	Ile	Ser	Glu	Pro	Arg	Ile	Ser	
		500						505					510			
Tyr	Gly	Asn	Asp	Ala	Leu	Met	Pro	Ser	Leu	Thr	Glu	Thr	Lys	Thr	Thr	
		515					520					525				
Val	Glu	Leu	Leu	Pro	Val	Asn	Gly	Glu	Phe	Ser	Leu	Asp	Asp	Leu	Gln	

530		535		540											
Pro	Trp	His	Ser	Phe	Gly	Ala	Asp	Ser	Val	Pro	Ala	Asn	Thr	Glu	Asn
545					550					555					560
Glu	Val	Glu	Pro	Val	Asp	Ala	Arg	Pro	Ala	Ala	Asp	Arg	Gly	Leu	Thr
				565						570					575
Thr	Arg	Pro	Gly	Ser	Gly	Leu	Thr	Asn	Ile	Lys	Thr	Glu	Glu	Ile	Ser
			580					585					590		
Glu	Val	Lys	Met	Asp	Ala	Glu	Phe	Arg	His	Asp	Ser	Gly	Tyr	Glu	Val
		595					600					605			
His	His	Gln	Lys	Leu	Val	Phe	Phe	Ala	Glu	Asp	Val	Gly	Ser	Asn	Lys
	610					615					620				
Gly	Ala	Ile	Ile	Gly	Leu	Met	Val	Gly	Gly	Val	Val	Ile	Ala	Thr	Val
625					630					635					640
Ile	Val	Ile	Thr	Leu	Val	Met	Leu	Lys	Lys	Lys	Gln	Tyr	Thr	Ser	Ile
				645					650					655	
His	His	Gly	Val	Val	Glu	Val	Asp	Ala	Ala	Val	Thr	Pro	Glu	Glu	Arg
		660					665					670			
His	Leu	Ser	Lys	Met	Gln	Gln	Asn	Gly	Tyr	Glu	Asn	Pro	Thr	Tyr	Lys
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Phe	Phe	Glu	Gln	Met	Gln	Asn									
	690					695									

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<212> PRT

<213> Artificial Sequence

<220>

<223> APP inhibitor peptide

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<222> 5

<223> Xaa = Sta = Statine

<400> 3

Ser Glu Val Asn Xaa Val Ala Glu Phe

1

5

<210> 4

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 4

gctctagaac ccagcacggc atccggctg

29

<210> 5

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

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42

<210> 6  
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<212> PRT  
<213> Artificial Sequence

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<223> Synthetically generated peptide

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<223> Xaa = Abz = amino benzoic acid

<221> VARIANT  
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<223> Xaa = = Dpa = 9,10-diphenylanthracene

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